

# Target genes for OBP3, a Dof transcription factor, include novel basic helix-loop-helix domain proteins inducible by salicylic acid

Hong-Gu Kang<sup>1,†,‡</sup>, Rhonda C. Foley<sup>2,†</sup>, Luis Oñate-Sánchez<sup>2</sup>, Chentao Lin<sup>1</sup> and Karam B. Singh<sup>1,2,\*</sup>

<sup>1</sup>Department of Molecular, Cell and Developmental Biology, University of California Los Angeles, 405 Hilgard Avenue, Los Angeles, CA 90095-1606, USA, and

<sup>2</sup>CSIRO, Plant Industry, Private Bag #5, Wembley, WA 6913, Australia

Received 7 February 2003; revised 24 April 2003; accepted 7 May 2003.

\*For correspondence (fax +61 8 9387 8991; e-mail karam.singh@csiro.au).

†Present address: Boyce Thompson Institute at Cornell University, Tower Road, Ithaca, NY 14850, USA.

‡These authors contributed equally to the paper.

## Summary

Overexpression of a salicylic-acid (SA)-inducible *Arabidopsis* DNA binding with one finger (Dof) transcription factor, called OBF-binding protein 3 (OBP3; AtDof3.6), has previously been shown to result in growth defects. In this study, suppressive subtraction hybridization (SSH) was used to isolate genes induced in an OBP3-overexpression line and several putative clones, called OBP3-responsive genes (*ORGs*), were isolated. The link with the induced expression levels of these genes and OBP3 overexpression was confirmed by analysing additional OBP3-overexpression lines. *ORG1* through *ORG4* are novel genes, while *ORG5* is an extensin gene, *AtExt1*. While *ORG4* has no similarity with other proteins in the database, *ORG1* has weak similarity in different regions of the predicted protein with CDC2 and fibrillin. *ORG2* and *ORG3* share 80% overall identity in their deduced amino acid sequences and contain a basic helix-loop-helix DNA-binding domain, suggesting that *ORG2* and *ORG3* may be transcription factors. The expression of the *ORG1*, *ORG2* and *ORG3* genes was co-regulated under all conditions examined including upregulation by SA and down-regulation by jasmonic acid (JA). Fifteen *OBP3*-silenced lines were generated to further explore the function of OBP3. Although there were no visible phenotypic changes in any of these lines, the expression of *ORG1*, *ORG2* and *ORG3* was reduced. Among the *ORG* genes, *ORG1*, *ORG2* and *ORG3* contained the highest number of potential Dof-binding sites in the promoter region, and their expression was significantly increased within 3 h after induction of OBP3 expression using an inducible promoter system, and closely reflected the expression levels of the exogenous OBP3 protein. The results from the gain-of-function and loss-of-function experiments suggest that the *ORG1*, *ORG2* and *ORG3* genes are direct target genes of OBP3.

**Keywords:** Dof, basic helix-loop-helix, salicylic acid, jasmonic acid, AtDof3.6.

## Introduction

Although there is considerable similarity in the regulation of transcription between animals and plants, there is growing evidence for transcription factor families that are unique to a particular kingdom. One class of transcription factors unique to plants is a novel type of zinc finger protein called DNA binding with one finger (Dof) proteins. Dof proteins contain a highly conserved 52-amino acid region called the Dof domain, which contains a single CX<sub>2</sub>CX<sub>2</sub>CX<sub>2</sub>C-type zinc finger motif (reviewed in Yanagisawa, 2002). The zinc finger in the Dof domain is essential for DNA binding as specific

mutations in cysteine residues within the zinc finger abolish DNA binding as do zinc chelators (see Yanagisawa, 2002 and references within). Binding sites for Dof proteins typically contain (A/T)AAAG or its complementary sequence (Yanagisawa and Schmidt, 1999). Some Dof proteins have also been shown to interact specifically with other types of transcription factors including bZIP proteins (Kang and Singh, 2000; Vincente-Carbajosa *et al.*, 1997; Zhang *et al.*, 1995), HMG1 (Yanagisawa, 1997), Myb proteins (Diaz *et al.*, 2002) and other Dof proteins (Yanagisawa, 1997).

Dof proteins have been isolated in a number of plant species by screens for DNA-binding proteins to specific promoter elements, by protein–protein interaction screening or by sequence homology (see Yanagisawa, 2002 and references within). As Dof proteins have only been found in plants, it has been speculated that they may play plant-specific roles. To date, Dof proteins have been implicated in seed-specific gene expression and seed germination (Diaz *et al.*, 2002; Gualberti *et al.*, 2002; Isabel-LaMoneda *et al.*, 2003; Mena *et al.*, 1998, 2002; Papi *et al.*, 2002; Vicente-Carabajosa *et al.*, 1997; Washio, 2001), the expression of genes involved in carbon metabolism (Yanagisawa, 2000; Yanagisawa and Sheen, 1998), response to plant hormones (Baumann *et al.*, 1999; De Paolis *et al.*, 1996), guard cell-specific gene expression (Plesch *et al.*, 2001) and plant defence/stress gene expression (Chen *et al.*, 1996; Kang and Singh, 2000). In some cases, closely related Dof proteins have been shown to have quite opposite functions. For example, the *Arabidopsis* DAG1 and DAG2 proteins play opposite regulatory roles in committing the seed to germinate (Gualberti *et al.*, 2002).

We have focused on a subgroup of the 37 *Arabidopsis* Dof proteins called OBF-binding proteins (OBPs; Kang and Singh, 2000; Zhang *et al.*, 1995). The first OBP protein (OBP1) was isolated as a protein that interacts with an ocs-element-binding factor, OBF4 (Zhang *et al.*, 1995). ocs elements are found in both pathogen and plant promoters, where they function as stress-responsive elements (see Singh *et al.*, 2002 and references within). While the OBP proteins showed similar *in vitro* DNA binding, protein–protein interaction and transcription-activation properties, they had distinct RNA-expression patterns with some family members showing a strong correlation with the activity of the ocs element (Kang and Singh, 2000). A range of phenotypes was observed in plants overexpressing OBP3, also called AtDof3.6, based on its chromosomal position (Yanagisawa, 2002). These phenotypes included retarded growth in both roots and aerial parts of the plant that, in the most severe cases, led to death (Kang and Singh, 2000).

To gain insight into the function of OBP3, we isolated genes induced in an OBP3-overexpression background using suppressive subtraction hybridization (SSH; Diatchenko *et al.*, 1996). Given that OBP3 is a DNA-binding protein with transcriptional activation activity, we reasoned that the phenotypes observed from OBP3-overexpression lines might result from constitutively expressing OBP3 target genes. Using SSH, five OBP3-responsive genes (ORGs) were isolated. Expression of three of these genes – *ORG1*, which encodes a protein of unknown function, and *ORG2* and *ORG3*, which encode closely related basic helix-loop-helix domain (bHLH) proteins – was co-regulated under all conditions examined, including upregulation by salicylic acid (SA) and downregulation by jasmonic acid (JA). To initiate loss-of-

function experiments with OBP3, we generated fifteen OBP3-silenced lines using intron-spliced hairpin (ihp) RNA. The OBP3-silenced lines had no visible phenotypic changes in contrast to what was seen with the OBP3-overexpression lines. However, the expression of the *ORG1*, *ORG2* and *ORG3* genes was reduced in the OBP3 silenced lines. *ORG1*, *ORG2* and *ORG3* expression was also significantly increased within 3 h after induction of OBP3 expression using an inducible promoter system, and closely reflected the expression levels of the exogenous OBP3 protein. Our results strongly suggest that the *ORG1*, *ORG2* and *ORG3* genes are direct target genes for OBP3.

## Results

### Screening for OBP3-responsive genes using suppressive subtraction hybridization

In an effort to identify induced genes in the OBP3-overexpressing plants, we used SSH. SSH was chosen for the following reasons: (i) SSH does not require very much plant tissue. This is important because the OBP3-overexpression lines are small in size and are difficult to propagate because of fertility problems. (ii) Low-abundance transcripts can be isolated with SSH. Total RNA from an OBP3-overexpression line and a wild-type line was isolated, and a cDNA library enriched for genes upregulated in an OBP3-overexpressing line was prepared. Differential screening of this library, which consisted of 198 clones with subtracted probes representing the OBP3-overexpressing line or the wild-type line, revealed a number of genes whose expression was enhanced in the OBP3 line. We initially focused on eight clones whose expression appeared to be upregulated the strongest in the OBP3 line. As shown in Table 1,

**Table 1** Isolation of OBP3-responsive genes (ORGs)

Genes	Frequency	Function	Gene locus	OBP-binding motifs (%)
ORG1	3	Unknown	At5g53450	9 (231)
ORG2	2	bHLH protein	At3g56970	10 (256)
ORG3	1	bHLH protein	At3g56980	10 (256)
ORG4	1	Unknown	At2g06010	7 (179)
ORG5	1	Extensin	At1g76930	5 (128)

This Table includes the frequency with which independent clones were isolated through suppressive subtraction hybridization (SSH), putative function of genes, gene locus, and number of OBP-binding motifs (CTTT (A/T) and (A/T)AAAG; Yanagisawa and Schmidt, 1999) located within 1-kb upstream of cDNA start site. Percentages in parentheses compare the number of OBP-binding motifs in the *ORG* promoter regions with the number of sites that is statistically expected from a 1-kb random sequence (less than four OBP-binding sites).

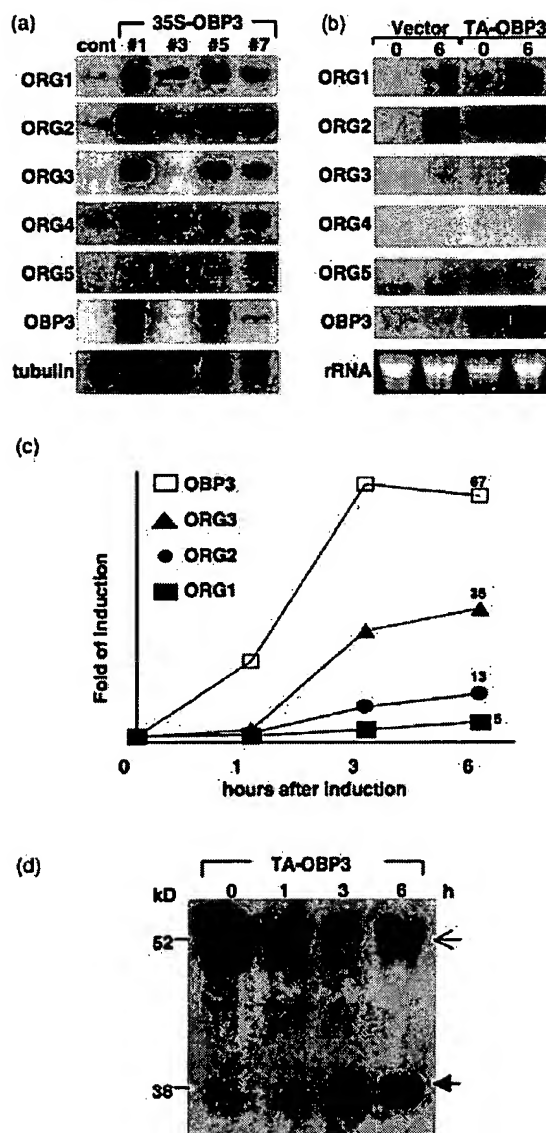
these clones were derived from five independent genes (*ORG1*–*ORG5*).

*OBP3-responsive gene expression correlates with the level of OBP3 expression in OBP3-overexpression lines under constitutive or inducible promoters*

The expression characteristics of the five genes were initially analysed using a virtual Northern blot analysis, and all the clones showed enhanced expression in the OBP3-overexpression background. The *ORG* gene induction by OBP3 was tested in three additional OBP3-overexpression lines – a strongly overexpressing OBP3 line (#1) similar to the original line used for the SSH screen (#5), an intermediate

OBP3 line (#7) and a weakly overexpressing OBP3 line (#3) – using RT-PCR, as shown in Figure 1(a). All the *ORG* genes were induced to different degrees in the OBP3-overexpression lines that had high or intermediate levels of *OBP3* transgene expression, with *ORG2* and *ORG4* showing the largest and the smallest induction, respectively. In contrast, in line #3 in which *OBP3* RNA levels were similar to that in the wild type, and where there were no significant effects on plant growth and development, there was also no change in *ORG* gene expression.

The OBP3-overexpression lines used in Figure 1(a) employed the constitutive cauliflower mosaic virus (CaMV) 35S promoter to express OBP3. We also checked the expression pattern of the *ORG* genes following an increase in OBP3 expression from a glucocorticoid-inducible promoter system (Aoyama and Chua, 1997; Kang *et al.*, 1999). The system consists of two components: a glucocorticoid-regulated chimeric transcription factor with the DNA-binding domain of the yeast transcription factor GAL4 called GVG, and the gene of interest transcribed from a promoter containing GAL4 DNA-binding sites. Transgenic plants containing the system only express the gene of interest following glucocorticoid treatment, as GVG is only activated upon binding glucocorticoid (for further details, see Aoyama and Chua, 1997). In Figure 1(b), expression of the *ORG* and *OBP* genes were analysed 6 h after the expression of OBP3 had been induced following treatment with dexamethasone (Dex), a chemical inducer for this system. We also examined *ORG* expression in a control line that



**Figure 1.** Analysis of OBP3-responsive gene (*ORG*) and OBP-binding protein 3 (*OBP3*) expression in OBP3-overexpression lines.

(a) RNA was isolated from four OBP3 transgenic lines under the control of the CaMV 35S promoter and control plants (cont) at the 12 to 16-day-old stage. Seedlings were grown on MS solid medium with kanamycin for 12 through 16 days. RT-PCR was performed using primers specific for each *ORG* gene. In the case of *OBP3* (exo), only the *OBP3* transgene was amplified.  $\beta$ -tubulin was used as a control for equal loading. The lane labelled cont is an unrelated kanamycin-resistant line that was used as a wild-type control for this experiment.

(b) RNA was isolated from a dexamethasone (Dex)-inducible line for OBP3 with/without induction. The line was grown for 3 weeks and then sprayed with 30  $\mu$ M of Dex. RNA was isolated from the lines before the induction (0) and 6 h after the induction (6). 25  $\mu$ g of RNA was used for Northern blot analysis, and rRNA stained with ethidium bromide was shown as a control for equal loading. In the case of *OBP3*, the *OBP3* transgene was shorter than the endogenous *OBP3* gene in size, resulting in two slightly different-sized bands.

(c) RT-PCR analysis with RNA isolated from a 3-week-old Dex-inducible line for OBP3 (TA-OBP3-#48) at 1, 3 and 6 h after treatment with 30  $\mu$ M of Dex. Expression levels were normalized to  $\beta$ -tubulin and the fold induction was graphed with 0 h serving as a reference point for each time point. The fold of induction at 6 h is shown next to each symbol.

(d) Immunoblot analysis with the same samples as used in (c). Monoclonal anti-hemagglutinin (HA) antibody was used to detect the exogenous OBP3 protein, which was tagged with an HA epitope (thick arrow). Cross-reacting Rubisco protein was used as a loading control (thin arrow). Approximately 20  $\mu$ g of protein was loaded into 12% SDS-PAGE, except for the 3-h time point which was underloaded. Size markers are shown on the left of the panel in kilodaltons.

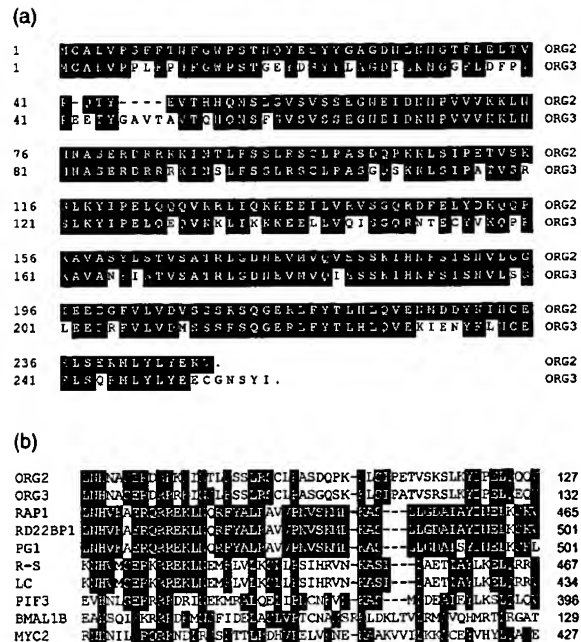
contained only the empty vector. *ORG1*, *ORG2* and *ORG3* showed a large increase in expression following induction of *OBP3*, whereas *ORG4* and *ORG5* had little to no change in expression. In the empty vector line, we also observed a small induction in *ORG1*, *ORG2* and *ORG3* expression, although the level of induction was considerably less than that observed in the *OBP3*-inducible line.

To determine if *OBP3* expression was enhanced before the increase in *ORG* expression, we examined earlier time points following Dex treatment. As shown in Figure 1(c), *OBP3* RNA levels had already increased significantly by 1 h, continued to increase at 3 h and appeared to have peaked by 6 h. In contrast, there was no change in *ORG* expression at 1 h, with an increase in expression of the three *ORG* genes first being observed at 3 h. *ORG* expression increased further at 6 h, although the induction appeared to be levelling off. The *OBP3* construct had been tagged with a hemagglutinin (HA) epitope and so changes in the levels of the exogenous *OBP3* protein following Dex treatment could be analysed. As shown in Figure 1(d), the increase in *OBP3* protein levels lagged a little behind the increase in RNA levels as expected, with little change at 1 h, but a significant increase by 3 h, when *ORG* RNA levels were first observed to have increased. Thus, the increase in expression of the *ORG1*, *ORG2* and *ORG3* genes follows soon after and parallels the increase in expression of *OBP3*, strongly suggesting that they are direct targets of *OBP3*.

The promoter regions of the *ORG* genes extending 1 kb from the cDNA start site were examined to see if they contain potential Dof-binding sites. As shown in Table 1, all five *ORG* genes contain multiple Dof-binding sites in this region, ranging from 10 for *ORG2* and *ORG3* to 5 for *ORG5*. The frequency of these Dof-binding sites was higher than the number that is statistically expected from a 1-kb random sequence, which would be less than 4. Interestingly, the three *ORG* genes (1, 2 and 3) that were significantly induced within 6 h when *OBP3* was expressed off an inducible promoter, also contained the highest number of potential Dof-binding sites in the promoter region.

#### Classification of the *OBP3*-responsive genes

One of the *ORG* genes had been previously characterized. *ORG5* is *AtExt1*, an extensin gene that codes for a class of hydroxyproline-rich glycoproteins that are abundant in plant cell walls (Merkouropoulos *et al.*, 1999). *ORG1*–*ORG4* are novel genes. While *ORG1*, *ORG2* and *ORG3* share some similarity with known genes, *ORG4* does not have any similarity with genes in the database. The *ORG1* gene comprises 13 exons and 12 introns and codes for a predicted protein of 670 amino acids. The *ORG1* protein appears to be novel, although database searches revealed weak similarity in different regions of the predicted *ORG1* protein with fibrillin proteins and some *cdc2* proteins.



**Figure 2.** *OBP3*-responsive gene 2 (*ORG2*) and *ORG3* are basic helix-loop-helix (bHLH) proteins.

(a) Alignment of predicted *ORG2* and *ORG3* full-length amino acid sequences.

(b) Alignment of the bHLH domain in *ORG2* and *ORG3* with bHLH proteins from different organisms ranging from plants to mammals. Accession numbers and origin species in parentheses for each gene are: RAP1 (*Arabidopsis*), X99548; RD22BP1 (*Arabidopsis*), AB000875; PG1 (bean), U18348; R-S (maize), P13027; LC (Maize), X57276; PIF3 (*Arabidopsis*), AAC95156; BMAL1B (human), AB000812; MYC2 (woodchuck), S11511. For both (a) and (b), identical amino acids are shown as white text on black box.

*ORG2* and *ORG3* were closely related to each other as shown in Figure 2(a), and have 79.8% overall identity in their deduced amino acid sequences. Both proteins contain a bHLH domain, which is known to be a DNA-binding domain present in plant and animal transcription factors. The alignment of the bHLH domains with other bHLH proteins from different organisms is shown in Figure 2(b). The deduced amino acid sequence of the bHLH domain in the *ORG2* and *ORG3* genes are diverged from other plant Myc proteins. In particular, three amino acids were inserted in the second helix region, which resembles animal Myc proteins more (compare BMAL1B and MYC2 with *ORG2* and *ORG3* in Figure 2b).

#### Salicylic and jasmonic acid responsiveness of the *OBP3*-responsive genes

As *OBP3* is an SA-responsive gene (Kang and Singh, 2000), we tested whether the novel *ORG* genes can also be induced by SA treatment. The SA-responsiveness of the *ORG* genes was analysed in aerial parts and roots

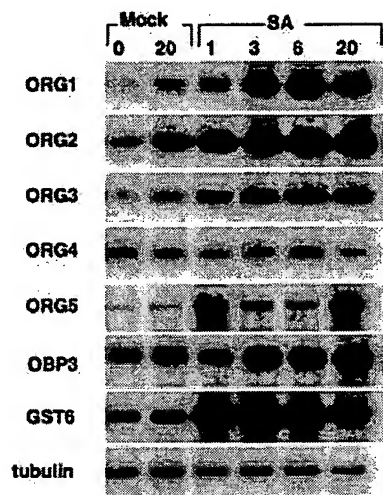


Figure 3. Analysis of *OBP3*-responsive gene (*ORG*) RNA levels following treatment with salicylic acid (SA).

Eight-day-old seedlings were transferred to fresh medium (mock) or medium that contained SA (100  $\mu$ M) for the indicated time in hours. RNA was then isolated from the roots and analysed using RT-PCR and primers specific for each gene. *GST6* also known as *GSTF8*, which is induced in response to SA, and  $\beta$ -tubulin were used as controls.

separately. As shown in Figure 3, *ORG1*, *ORG2* and *ORG3*, like *OBP3*, were SA-inducible in roots, while *ORG4* did not respond to SA within the time period tested. None of the *ORG* genes showed significant SA responses in aerial tissue (data not shown), similar to what was seen with *OBP3* (Kang and Singh, 2000).

The RNA expression patterns of *OBP3* and the SA-inducible *ORG* genes were analysed in two different *Arabidopsis* mutants, *cpr5-2* (Bowling *et al.*, 1997) and *cep1* (Silva *et al.*, 1999), which constitutively express plant-defence responses. The *CPR5* gene encodes a novel, putative transmembrane protein (Kirik *et al.*, 2002), and *cpr5-2* plants have elevated levels of SA, enhanced levels of *PR1*, increased *PDF1.2* gene expression and enhanced resistance to virulent strains of *Pseudomonas syringae* and *Peronospora parasitica* (Bowling *et al.*, 1997). The *cep1* mutant has higher levels of SA as well as higher levels of *PR* and *PDF1.2* gene expression (Silva *et al.*, 1999; Oñate-Sánchez and Singh, 2002). As shown in Figure 4(a), there was no difference in the expression levels of *OBP3* or *ORG1*, *ORG2* and *ORG3* between the wild type and the *cpr5-2* mutant, while there was a clear induction of *PR5* and *PDF1.2* expression, which are SA- and JA-responsive genes, respectively. While there was again no difference in the expression of *OBP3* between the wild-type plants and the *cep1* mutant, there was a significant reduction in *ORG1*, *ORG2* and *ORG3* expression in this mutant background.

As the high levels of *PR5* and *PDF1.2* expression in the *cpr5-2* and *cep1* mutants suggest activated SA- and JA-

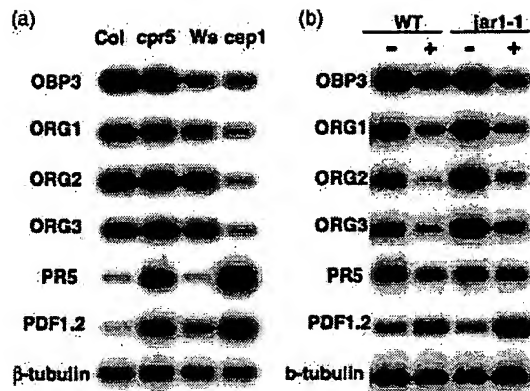


Figure 4. Analysis of *OBP3*, *ORG1*, *ORG2* and *ORG3* RNA levels in mutants with altered responses to defence-signaling molecules and/or pathogens. (a) RT-PCR analysis of RNA samples from 2-week-old *Arabidopsis* seedlings of the Columbia (Col) or Wassilewskija (Ws) ecotype and *cpr5-2* (Bowling *et al.*, 1997) and *cep1* (Silva *et al.*, 1999) mutants. *PR5* and *PDF1.2*, which are upregulated by salicylic acid (SA; Ward *et al.*, 1991) and methyl jasmonate (MeJA; Penninckx *et al.*, 1998), respectively, were used as controls. (b) RT-PCR analysis of RNA samples from 2-week-old *Arabidopsis* seedlings of the Columbia (WT) ecotype and the *jar1-1* mutant (Staswick *et al.*, 1998) treated for 6 h with 0.1% (v/v) ethanol (-) or 100  $\mu$ M MeJA solution in 0.1% (v/v) ethanol (+).

signalling pathways, we analysed the expression of *OBP3*, and *ORG1*, *ORG2* and *ORG3* after treatment with MeJA in a JA-resistant mutant, *jar1-1* (Staswick *et al.*, 1998). JAR1 appears to belong to the acyl adenylate-forming firefly luciferase superfamily (Staswick *et al.*, 2002) and *jar1-1* plants have decreased sensitivity to JA inhibition of root elongation and are more susceptible to the soil fungus *Pythium irregulare* (Staswick *et al.*, 1992, 1998). As shown in Figure 4(b), the expression of both *OBP3* and the *ORG1*, *ORG2* and *ORG3* genes were repressed in response to MeJA in the wild type and the *jar1-1* mutant. *PDF1.2* gene expression was used as a control for the MeJA treatment, and its expression was induced both in the wild type and in the *jar1-1* mutant as seen previously by Oñate-Sánchez and Singh (2002).

#### *ORG1* to *ORG3* RNA levels are decreased in *OBP3*-silenced lines

We initiated loss-of-function experiments using gene constructs encoding ihpRNA (Wesley *et al.*, 2001) against *OBP3* to further analyse the function of *OBP3* and the role it plays in regulating the expression of the *ORG1*, *ORG2* and *ORG3* genes. The ihp*OBP3* construct contained 525 bp of *OBP3*-specific sequence as determined by BLAST search against the *Arabidopsis* genome. Fifteen independent lines were generated, and none of these lines had any visible phenotype. Seven of these lines contained single T-DNA-insertion sites as determined by segregation analysis, and we focused on these lines. T<sub>3</sub> lines were further characterized

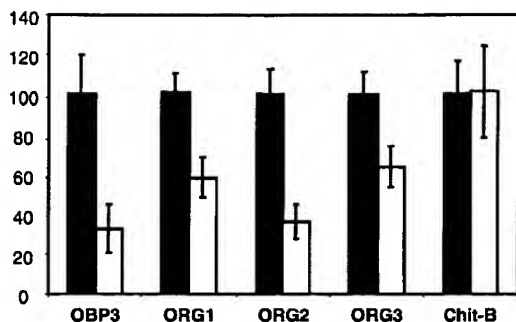


Figure 5. OBP3-responsive gene 1 (*ORG1*), *ORG2* and *ORG3* RNA levels are reduced in OBP3-silenced lines.

RNA was isolated from seedlings from seven independent lines and five wild-type (Columbia) replicates grown on MS solid medium for 8 days. RT-PCR was performed using primers specific for *OBP3*, *ORG1*, *ORG2*, *ORG3*, *OBP3* and *chitinase*, and normalized to  $\beta$ -tubulin. The relative average with wild type set at 100% and standard error of the five wild-type replicates (black columns) and seven independent hpOBP3 lines (white columns) are graphed.

by RT-PCR. As shown in Figure 5, the ihpOBP3 lines contained on average approximately 30% OBP3 RNA compared to the wild type. These ihpOBP3 lines also had reduced levels of *ORG1*, *ORG2* and *ORG3*. *Chitinase B* was used as a control to show that the reduction in *ORG1*, *ORG2* and *ORG3* expression was a specific effect and not a general stress response. These results are consistent with the results obtained with the OBP3-overexpressing lines under constitutive or inducible promoters, and show that the expression of *ORG1*, *ORG2* and *ORG3* is strongly correlated with OBP3 expression.

## Discussion

To gain insight into the function of OBP3 *in planta*, we screened for genes that are induced in an OBP3-overexpression line using SSH, a cDNA subtraction method. One of the *ORG* genes, *ORG4*, encodes for an unknown protein, while another, *ORG5/AtExt1*, is an *Arabidopsis* extensin gene (Merkouropoulos *et al.*, 1999). Extensins are hydroxyproline-rich glycoproteins that are very abundant in plant cell walls where they may function to increase the mechanical strength of the cell wall (see Bucher *et al.*, 2002; Kieliszewski and Lamport, 1994). Extensins may also be involved in plant-defence responses as pathogen infection and treatment with elicitors has been shown to induce their expression (Benhamou *et al.*, 1990; Corbin *et al.*, 1987; Mazau and Esquerre-Tugaye, 1986; Showalter *et al.*, 1985). *ORG5/AtExt1* was shown previously to be induced by SA, wounding and other defence-related compounds such as MeJA (Merkouropoulos *et al.*, 1999).

The other three *ORG* genes encode proteins with similarity to other proteins in the database. *ORG1* has weak similarity in different regions of the protein to fibrillin

proteins, which are major components of the extracellular microfibrils, and some cdc2 proteins, which are involved in cell-cycle control. However, no clones with similarity to both cdc2 and fibrillin genes were present in the database, indicating that *ORG1* may represent a novel class of genes. Although the region of highest similarity between *ORG1* (230–302 amino acids) and the rice CDC2 protein (102–174 amino acids) scores 49% similarity with 30% amino acids being identical, *ORG1* lacks the signature motifs of the cdc2 protein family: the PSTAIR motif (EGVP-STAIRISLLKE; 42–57 amino acids in the yeast CDC2), which binds to a cyclin, and the GEGTYG motif (GEGTYG: 11–16 amino acids in the yeast CDC2), which is in the amino-terminal ATP-binding domain. Therefore, it is not clear whether *ORG1* has a cell cycle regulatory function merely based on the amino acid similarity, and further work will be required to address this question.

*ORG2* and *ORG3* both encode proteins that contain a bHLH domain, share approximately 80% overall identity, are located next to each other in the genome and are responsive to SA with similar kinetics to *OBP3*. Myc proteins with a bHLH domain have been shown to be potent inducers of both cell proliferation and apoptosis in animals (see Eisenman, 2001 and Pelengaris *et al.*, 2000 for reviews). Plant Myc homologs appear to function in a number of different areas. For example, in maize, the Myc proteins encoded by the *R*-gene family including the *R*, *Lc*, *B* and *Sn* proteins regulate the anthocyanin biosynthesis pathway. Another plant Myc-like protein is the *Arabidopsis* RD22BP1 protein, which is induced by ABA, a stress signal in plants, and by dehydration stress (Abe *et al.*, 1997). It is noteworthy that the deduced amino acid sequence of the bHLH domain in *ORG2* and *ORG3* are diverged from other plant Myc-like proteins, suggesting that the *ORG2* and *ORG3* DNA-binding profiles and function may be different from these proteins.

The expression patterns of the *ORG1*, *ORG2* and *ORG3* genes were very similar in all the situations examined. All three genes were coordinately induced in an OBP3-inducible line within 3 h following treatment with the chemical inducer Dex, although the absolute levels of induction differed. The increase in *ORG1*, *ORG2* and *ORG3* expression occurred shortly after *OBP3* RNA levels started to increase, and closely reflected the expression levels of the exogenous OBP3 protein. The *ORG1*, *ORG2* and *ORG3* genes also showed a small induction in an empty vector line following treatment with Dex, although the levels of induction were small compared to the OBP3-inducible line. The expression of some stress-responsive genes (*PDF1.2* and *PR-5*) has also been shown to be induced in empty vector lines following Dex treatment, although in these cases, induction was observed later, 24 or 48 h after Dex treatment (Kang *et al.*, 1999).

The *ORG1*, *ORG2* and *ORG3* genes were also inducible by SA and downregulated by JA. The interaction between the

SA and JA signalling pathways is known to be complex with both antagonistic and synergistic interactions reported (reviewed in Glazebrook, 2001), for example, a SA-responsive *PR1* gene was repressed by JA (Rao *et al.*, 2000). In another study, 8 out of 2300 genes were found to be induced by SA and repressed by JA using microarray hybridizations (Schenk *et al.*, 2000). However, antagonistic response to these hormones is clearly not universal, as Schenk *et al.* (2000) also found that a significantly higher number of genes were co-induced or co-repressed by SA and JA. Interestingly, the expression of the *ORG1*, *ORG2* and *ORG3* genes was not affected in the *cpr5-2* mutant and even reduced in the *cep1* mutant, although both mutants are known to have elevated SA levels (Bowling *et al.*, 1997; Silva *et al.*, 1999).

*OBP3* was also often expressed in a similar manner to the *ORG1*, *ORG2* and *ORG3* genes. One exception was in *cep1*, where the expression of *OBP3* was not affected, while the expression of the *ORG1*, *ORG2* and *ORG3* genes was significantly reduced. Moreover, while the induction of *OBP3* by SA is not reduced by cycloheximide (Kang and Singh, 2000), this is not the case with *ORG1* (our unpublished observation). These results demonstrate that *OBP3* is not co-regulated with the *ORG1*, *ORG2* and *ORG3* genes and are consistent with *OBP3* being upstream of *ORG* regulation, and that other unknown factors also influence *ORG*-expression levels.

The transgenic lines overexpressing *OBP3* under the control of the CaMV 35S promoter had a range of phenotypes, the severity of which correlated with the levels of *OBP3* expression (Kang and Singh, 2000). These phenotypes included growth defects involving retarded growth in both roots and aerial parts of the plant. In the most severe cases, these growth defects led to death. At this stage, it remains unclear whether one or more of the *ORGs* isolated in this study contributed to any of these phenotypes. *ORG1* and *ORG4* encode proteins of unknown function, and *ORG2* and *ORG3* encode potential transcription factors but where the identity of target genes is unknown. In the case of *ORG5*, overexpression or antisense repression of other extensin genes did not give rise to any visible phenotypes (Bucher *et al.*, 2002; Memelink *et al.*, 1993).

In contrast to the *OBP3*-overexpressing lines, the *OBP3*-silenced lines had no obvious visible phenotypes, although they did lead to specific changes in gene expression. One possibility is that other proteins such as *OBP1* and/or *OBP2*, which are also responsive to SA and have similar DNA-binding and protein-protein interaction properties as *OBP3* (Kang and Singh, 2000), may be able to compensate for the reduction in *OBP3* expression. It will be interesting to examine if the *ORG* genes are affected in other *OBP*-mutant backgrounds. Another possibility is that complete silencing of *OBP3* was not achieved with the *ihpRNA* approach (Wesley *et al.*, 2001). Although this silencing approach

was shown to result in well over 80% suppression of target genes tested (Wesley *et al.*, 2001), we have failed to obtain similarly efficient silencing lines not only for *OBP3*, but also for other transcription factors including *TGA2* (Kang *et al.*, unpublished results). The difficulty to get efficient silencing lines for *OBP3* may be as a result of lethality caused from the loss of *OBP3*.

The promoter regions of the *ORG* genes were examined, and were found to contain a higher frequency of potential Dof-binding sites than statistically expected for a random sequence of the same size. For example, the *ORG2* and *ORG3* promoter regions each had ten Dof-binding sites and the *ORG1* promoter region had nine sites, whereas a random sequence would be predicted to have less than four. Other gene promoters have also been shown to contain multiple Dof-binding sites, including the maize *cypdk1* promoter (Yanagisawa, 2000), the *Arabidopsis* *GST6* promoter (Chen *et al.*, 1996) and the potato *KST1* promoter (Plesch *et al.*, 2001). With whole-genome sequences available for some model systems, it was proposed that genes regulated by a transcription factor could be identified by a cluster of the corresponding binding sites (Wagner, 1999). Computational methods looking for a cluster of transcription-factor-binding sites more frequent than expected by chance alone revealed downstream genes for several transcription factors in *Drosophila* (Berman *et al.*, 2002; Rebeiz *et al.*, 2002). Moreover, microarray analysis of systemic acquired resistance (SAR)-induced genes in *Arabidopsis* showed that W-boxes, binding sites for WRKY transcription factors, are highly enriched in the promoter regions (Maleck *et al.*, 2000). These results suggest that the clustering of binding sites for some transcription factors could be a common scheme for gene regulation. Interestingly, all three *ORG* genes whose expression was significantly increased in the *OBP3*-inducible lines, also had the highest frequency of Dof-binding sites in the promoter region. However, which of these Dof-binding sites in the *ORG* promoters are functional remains to be determined.

The combined results of the gain-of-function and loss-of-function experiments strongly suggest that the *ORG1*, *ORG2* and *ORG3* genes are direct target genes of *OBP3*. Thus, some of the direct target genes of *OBP3* may encode regulatory factors. Further studies will be required to determine the function of the *ORG1*, *ORG2* and *ORG3* genes and the role they play in the growth defects observed in *OBP3*-overexpressing lines.

## Experimental procedures

### Plant materials, growth conditions and treatments

*Arabidopsis thaliana* (ecotype Columbia) seeds were surface sterilized with 70% ethanol for 15 min, dried on autoclaved paper, stratified at 4°C for 2 days and grown on MS (Sigma, St Louis, MO,



USA) medium or on autoclaved soil. Plants were grown at 22°C with a day length of 16 h. For treatments with MeJA and SA, *Arabidopsis* seedlings were grown on MS solid medium for 8 days. The plants were treated in MS liquid medium containing 100  $\mu\text{M}$  SA (Sigma) or 100  $\mu\text{M}$  MeJA (Aldrich, Milwaukee, WI, USA). Total seedlings or roots of the plants were collected and frozen in liquid nitrogen prior to RNA isolation. For Dex treatment, *Arabidopsis* seeds were germinated on MS solid medium with 20  $\mu\text{g ml}^{-1}$  hygromycin B to select transgenic lines. After 1 week on the MS medium, seedlings were transferred to autoclaved soil and grown for two more weeks. 30- $\mu\text{M}$  Dex solution in 0.01% Tween-20 was sprayed onto seedlings, which were then subjected to a vacuum treatment for 2 min. The plants were collected and frozen in liquid nitrogen prior to RNA isolation.

*Preparation of double-strand cDNAs for RACE (rapid amplification of cDNA ends), virtual Northern blot, and suppression subtractive hybridization*

One microgram of cDNA was denatured with 10 pmol of the following primers in 5  $\mu\text{l}$  of total volume at 72°C for 2 min and cooled at 4°C for 2 min: cDNA synthesis primers (5'-AAGCAGTGGTAACAACGAGAGTACT<sub>30</sub>N<sub>3</sub>-3') and SMARTII oligonucleotide (5'-AAGACGTGGTAACAACGCAGATGTACGCGGG-3'). A mixture containing 2  $\mu\text{l}$  of the supplied buffer (Gibco BRL, Rockville, MD, USA), 20 nmol of DTT, 10 nmol of dNTP and 200 units of MMLV reverse transcriptase (Gibco) in 10  $\mu\text{l}$  final volume was added and incubated at 42°C for 1 h, followed by addition of 40  $\mu\text{l}$  of TE (10 mM Tris (pH 7.6), 1 mM EDTA). The synthesized double-strand cDNA was then heat-denatured at 72°C for 7 min and stored at -80°C.

One microlitre of double-stranded cDNA, synthesized as described in the previous section, was amplified in a final volume of 20  $\mu\text{l}$ , which contained 10 nmol of dNTP, 1 $\times$  Advantage2 polymerase mix (Clontech, Palo Alto, CA, USA), the supplied buffer (Clontech) and the following primers synthesized specific to the gene of interest. This primer was designed to bind to the junction of two consecutive exons (this suppresses an amplification from genomic DNA).

In the case of 3' RACE, 10 pmol of oligo dT<sub>18</sub> was used and for 5' RACE, a mixture of two primers (0.2 pmol of 5'-CTAATACGACTCACTATAGGGCAAGCAGTGGTAACAACGAGAGT-3' and 1 pmol of 5'-CTAATACGACTCACTATAGGGC-3') was used. The following PCR programme was used: 5 cycles of 94°C for 5 sec and 72°C for 3 min, followed by 5 cycles of 94°C for 5 sec, 70°C for 10 sec and 72°C for 3 min, and again followed by 27 cycles of 94°C for 5 sec, 68°C for 10 sec and 72°C for 3 min. In the case of 3' RACE, the PCR products were then subcloned into an appropriate vector and sequenced. In the case of 5' RACE, 0.1  $\mu\text{l}$  of the PCR products was subsequently amplified with a secondary PCR in a final volume of 20  $\mu\text{l}$  that contained 10 nmol of dNTP, 1 $\times$  Advantage2 polymerase mix (Clontech), the provided buffer (Clontech), 10 pmol of the nested primer for 5' cDNA end (5'-AAGCAGTGGTAACAACGAGAGT-3') and 10 pmol of the nested primer for the gene of interest. The following PCR programme was used: 25 cycles of 94°C for 5 sec, 68°C for 10 sec and 72°C for 3 min. The PCR product was then cloned and sequenced.

One microliter of double-strand cDNA was amplified with a mixture containing 1 $\times$  Advantage 2 polymerase mix (Clontech), the supplied buffer (Clontech), 20 nmol of dNTP, 20 pmol of PCR primer (5'-AAGCAGTGGTAACAACGAGAGT-3') in a final volume of 100  $\mu\text{l}$  using the following PCR programme: 95°C for 1 min, followed by 20–25 cycles of 95°C for 5 sec, 65°C for 5 sec and 68°C for 6 min (for SSH, two identical reactions were performed to

obtain enough material for the subsequent step). The amplification was stopped before the PCR reached the saturation phase: this was checked by aliquotting PCR samples at different cycles. 2  $\mu\text{l}$  of 0.5M EDTA was added to terminate the PCR reactions. 10  $\mu\text{l}$  of the amplified products were then loaded on a 1.5% agarose gel for a virtual Northern analysis, followed by the standard procedure for Southern blot analysis (Sambrook *et al.*, 1989).

Two hundred microliters of amplified products from a virtual Northern blot analysis was purified using Concert Rapid PCR Purification System (Gibco) according to the manufacturer's instruction, resulting in a 50- $\mu\text{l}$  TE solution. The solution was then digested with 30 units of *RsaI* in 300  $\mu\text{l}$  final volume at 37°C for 4 h, followed by purification using Concert Rapid PCR Purification System (Gibco) according to the manufacturer's instruction, resulting in a 50- $\mu\text{l}$  TE solution. The solution was then precipitated with 2 volumes of 100% ethanol and 0.1 volume of 3 M sodium acetate (pH 5.2) and resuspended to 0.3  $\mu\text{g } \mu\text{l}^{-1}$  with water. The digested double-stranded cDNA was then used for SSH, using the PCR-Select cDNA Subtraction Kit (Clontech) according to the manufacturer's instruction. The resulting products from the PCR-Select cDNA Subtraction Kit (Clontech) were subcloned into the pT-Adv vector (Advantage PCR cloning kit, Clontech). Plasmid DNAs of pT-Adv containing each product from the hybridization were prepared and used in a dot-blot analysis to screen for differentially expressed clones using a standard protocol (Sambrook *et al.*, 1989).

*Generation of hpOBP3 lines*

To produce hairpin constructs, a 525-bp OBP3 fragment was amplified using the following primers: 5'-GGGGATCGATGGTACCTGATAATACTACTAGTA-3' and 5'-GGGTCTAGACTCGAGGCTGTGAGTTGTTGG-3'. The PCR product was digested with the appropriate restriction enzymes, purified and ligated into the *XbaI/Clal* site and the *XhoI/KpnI* site of pHANNIBAL (Wesley *et al.*, 2001). The *NotI* cassette was then transferred to the binary vector pART27. *Arabidopsis* was transformed with this construct using standard infiltration techniques and selection for kanamycin-resistance.

*RNA Isolation, Northern and RT-PCR analysis*

Total RNA was isolated from *Arabidopsis*, using the Purescript reagent (Gentra Systems, Minneapolis, MN, USA) according to the manufacturer's instruction, except for the protein precipitation step in which RNA samples were centrifuged twice instead of once. Purified RNA for RT-PCR analysis was subject to further purifications: Purified RNA was treated with 2 units of RNase-free DNase (Promega, Madison, WI, USA) at 37°C for 60 min and was re-purified again with the Purescript reagent (Gentra Systems).

Northern blot analysis and synthesis of random primed probes were performed as described earlier (Shah *et al.*, 1999). Random primed probes were synthesized from PCR fragments from *Arabidopsis* cDNA with oligonucleotides used for RT-PCR. Northern gel blot hybridization was performed as described previously by Kachroo *et al.* (1995).

For cDNA synthesis, 1  $\mu\text{g}$  of RNA in 5  $\mu\text{l}$  of the total volume was denatured at 65°C for 10 min and mixed with 0.5  $\mu\text{g}$  of oligo dT<sub>18</sub>, 12 nmol of dNTP, 2 units of AMV reverse transcriptase (Promega) and 10 units of RNase inhibitor (Promega) in 25  $\mu\text{l}$  of the supplied buffer. The mixture was then incubated at 37°C for 1 h, denatured at 65°C for 10 min and stored at -80°C until the PCR reactions were performed.

All PCR reactions were performed with an annealing temperature of 60°C, 0.5 unit of Taq polymerase (Invitrogen, Carlsbad, CA, USA), 4 nmol of dNTP and a pair of primers (10 pmol each) in a



final volume of 20 µl of the buffer recommended by the supplier. For each primer condition, the cycle was chosen as two cycles prior to visualization on an ethidium bromide-stained agarose gel. The following are the specific primer pairs used for the RT-PCR: Numbers in parentheses indicate the number of PCR cycles completed for each target gene.

- ORG1 (22): 5'-CCTTGTACATGGGTGCCATGGAAGT-3'  
5'-ACTGTAAGCGTTGCTAGTACTTGG-3'
- ORG2 (20): 5'-ACCACAGACTTATGAAGTGA-3'  
5'-CCGATACTCGTACCAAAATT-3'
- ORG3 (22): 5'-TGGAGCTGTTACAGCGGTGA-3'  
5'-CTGAAATTTGCACCAAGAGC-3'
- ORG4 (22): 5'-CAATAACCTTGTCTTGTATTAAGC-3'  
5'-AGACATGAACGGAGAGATGAGAAC-3'
- ORG5 (23): 5'-ATGGCCTCTTCTTGTCTTAGCA-3'  
5'-CCATTAGAGACGATTAAGTAATCTA-3'
- GST6 (15): 5'-CCCCGTCGATGAGAGC-3'  
5'-GAGAGAGGGTCACTACTGCTTCTGG-3'
- OBP3 (26): 5'-AGTAAGGGAACCAACATCAG-3'  
5'-GCTTGAGTCACATCTAGGGC-3'
- Chitinase (22): 5'-CGGTGGTACTCTCTGGACCCACCGGC-3'  
5'-CGGCGGCACGGTCGGCGTCTGAAGGCTG-3'
- β-tubulin (20): 5'-ATCACAGCAATACAGAGCCTTAACC-3'  
5'-GCTGTTGTTATTGCTCCTCTGCA-3'
- PR5 (20): 5'-ATGGCAAATATCTCCAGTATTCACA-3'  
5'-ATGTCGGGGCAAGCCGCTTGAGG-3'
- PDF1.2 (27): 5'-AATGGATCCATGGCTAAGTTTGCTTCCATC-3'  
5'-AATGAATTCATACACACGATTTAGCACC-3'

The PCR products were run on a 1.5–2% agarose gel, transferred to a nylon membrane (Bio-Rad, Hercules, CA, USA) and probed with the corresponding random-primed <sup>32</sup>P-labelled probe. Amplification products were imaged using a Storm 840 phosphorimager (Molecular Dynamics, Sunnyvale, CA, USA) or Cyclone phosphorimager (Packard, Meriden, CT, USA). IMAGEQUANT software (Molecular Dynamics) with the default parameters was used for quantizing RT-PCR products.

#### Immunoblot analysis

Immunoblot was analysed as described previously using an enhanced chemiluminescence method (Amersham, Pharmacia Biotech, Piscataway, NJ, USA; Lin *et al.*, 1995) with the following modification. The blot, a PVDF membrane (Millipore, Bedford, MA, USA), was probed with anti-HA antibody (Sigma, diluted 1/1000) and then with anti-mouse antibody conjugated to horseradish peroxidase (Sigma, diluted 1/5000).

#### Acknowledgements

We thank Louise Thatcher and John Klingler for helpful comments on the manuscript, Elaine Smith and Pradeep Kachroo for excellent technical help and other members of the Singh and Lin labs for helpful discussions. We also thank the Nottingham Arabidopsis Stock Centre for providing the seeds for *cep1*, *cpr5-2* and *jar1-1*. H.K. was supported in part by a pre-doctoral fellowship from the Korean Ministry of Education. This work was supported in part by a grant from the US Department of Agriculture to K.B.S. (96-35100-3165).

#### References

Abe, H., Yamaguchi-Shinozaki, K., Urao, T., Iwasaki, T., Hosokawa, D. and Shinozaki, K. (1997) Role of *Arabidopsis* MYC and MYB

homologs in drought- and abscisic acid-regulated gene expression. *Plant Cell*, **9**, 1859–1868.

- Aoyama, T. and Chua, N.H. (1997) A glucocorticoid-mediated transcriptional induction system in transgenic plants. *Plant J.* **11**, 605–612.
- Baumann, K., De Paolis, A., Costantino, P. and Gualberti, G. (1999) The DNA binding site of the Dof protein NtBBF1 is essential for tissue-specific and auxin-regulated expression of the rolB oncogene in plants. *Plant Cell*, **11**, 323–334.
- Benhamou, N., Mazau, D. and Esquerre-Tugaye, M.D. (1990) Immuno-cytochemical localisation of hydroxyproline-rich glycoproteins in tomato root cells infected by *Fusarium oxysporum* f. sp. *radici-lycopersici*: study of a compatible interaction. *Mol. Plant Pathol.* **80**, 163–173.
- Berman, B.P., Nibu, Y., Pfeiffer, B.D., Tomancak, P., Celniker, S.E., Levine, M., Rubin, G.M. and Eisen, M.B. (2002) Exploiting transcription factor binding site clustering to identify cis-regulatory modules involved in pattern formation in the *Drosophila* genome. *Proc. Natl. Acad. Sci. USA*, **99**, 757–762.
- Bowling, S.A., Clarke, J.D., Liu, Y., Klessig, D.F. and Dong, X. (1997) The *cpr5* mutant of *Arabidopsis* expresses both NPR1-dependent and NPR1-independent resistance. *Plant Cell*, **9**, 1573–1584.
- Bucher, M., Brunner, S., Zimmermann, P., Zardi, G.I., Amrhein, N., Willmitzer, L. and Riesmeier, J.W. (2002) The expression of an extensin-like protein correlates with cellular tip growth in tomato. *Plant Physiol.* **128**, 911–923.
- Chen, W., Chao, G. and Singh, K.B. (1996) The promoter of a H<sub>2</sub>O<sub>2</sub>-inducible, *Arabidopsis* glutathione S-transferase gene contains closely linked OBF- and OBP1-binding sites. *Plant J.* **10**, 955–966.
- Corbin, D.R., Sauer, N. and Lamb, C.J. (1987) Differential regulation of a hydroxyproline-rich glycoprotein gene family in wounded and infected plants. *Mol. Cell Biol.* **7**, 4337–4344.
- De Paolis, A., Sabatini, S., De Pascalis, L., Costantino, P. and Capone, I. (1996) A rolB regulatory factor belongs to a new class of single zinc finger plant proteins. *Plant J.* **10**, 215–223.
- Diatchenko, L., Lau, Y.F., Campbell, A.P. *et al.* (1996) Suppression subtractive hybridization: a method for generating differentially regulated or tissue-specific cDNA probes and libraries. *Proc. Natl. Acad. Sci. USA*, **93**, 6025–6030.
- Diaz, I., Vicente-Carbajosa, J., Abraham, Z., Martinez, M., Isabel-La Moneda, I. and Carbonero, P. (2002) The GAMBY protein from barley interacts with the DOF transcription factor BPBF and activates endosperm-specific genes during seed development. *Plant J.* **29**, 453–464.
- Eisenman, R.N. (2001) Deconstructing myc. *Genes Dev.* **15**, 2023–2030.
- Glazebrook, J. (2001) Genes controlling expression of defense responses in *Arabidopsis* – 2001 status. *Curr. Opin. Plant Biol.* **4**, 301–308.
- Gualberti, G., Papi, M., Bellucci, L., Ricci, I., Bouchez, D., Camilleri, C., Costantino, P. and Vittorioso, P. (2002) Mutations in the Dof zinc finger genes *DAG2* and *DAG1* influence with opposite effects the germination of *Arabidopsis* seeds. *Plant Cell*, **14**, 1253–1263.
- Isabel-LaMoneda, I., Diaz, I., Martinez, M., Mena, M. and Carbonero, P. (2003) SAD: a new DOF protein from barley that activates transcription of a cathepsin B-like thiol protease gene in the aleurone of germinating seeds. *Plant J.* **33**, 329–340.
- Kachroo, P., Leong S.A. and Chattoo, B.B. (1995) Mg-SINE: a short interspersed nuclear element from the rice blast fungus

- Magnaporthe grisea*. *Proc. Natl. Acad. Sci. USA*, **92**, 11125–11129.
- Kang, H., Fang, Y. and Singh, K.B. (1999) A glucocorticoid-inducible transcription system causes severe growth defects in *Arabidopsis* and induces defense-related genes. *Plant J.* **20**, 127–133.
- Kang, H.G. and Singh, K.B. (2000) Characterization of salicylic acid-responsive, *Arabidopsis* Dof domain proteins: overexpression of OBP3 leads to growth defects. *Plant J.* **21**, 329–339.
- Kieliszewski, M.J. and Lampion, D.T. (1994) Extensin: repetitive motifs, functional sites, post-translational codes, and phylogeny. *Plant J.* **5**, 157–172.
- Kirik, V., Bouyer, D., Schobinger, U., Bechtold, N., Herzog, M., Bonneville, J.M. and Hulskamp, M. (2001) CPR5 is involved in cell proliferation and cell death control and encodes a novel transmembrane protein. *Curr. Biol.* **27**, 1891–1895.
- Lin, C., Ahmad, M., Gordon, D. and Cashmore, A.R. (1995) Expression of an *Arabidopsis* cryptochrome gene in transgenic tobacco results in hypersensitivity to blue, UV-A, and green light. *Proc. Natl. Acad. Sci. USA*, **92**, 8423–8427.
- Maleck, K., Levine, A., Eulgem, T., Morgan, A., Schmid, J., Lawton, K.A., Dangel, J.L. and Dietrich, R.A. (2000) The transcriptome of *Arabidopsis thaliana* during systemic acquired resistance. *Nat. Genet.* **26**, 403–410.
- Mazau, D. and Esquerre-Tugaye, M.D. (1986) Hydroxyproline-rich glycoprotein accumulation in the cell walls of plants infected by various pathogens. *Physiol. Mol. Plant Pathol.* **29**, 147–157.
- Memelink, J., Swords, K.M., de Kam, R.J., Schilperoort, R.A., Hoge, J.H. and Staehelin, L.A. (1993) Structure and regulation of tobacco extensin. *Plant J.* **4**, 1011–1022.
- Mena, M., Vicente-Carbajosa, J., Schmidt, R.J. and Carbonero, P. (1998) An endosperm-specific DOF protein from barley, highly conserved in wheat, binds to and activates transcription from the prolamin-box of a native B-hordein promoter in barley endosperm. *Plant J.* **16**, 53–62.
- Mena, M., Cejudo, F.J., Isabel-Lamonedá, I. and Carbonero, P. (2002) A role for the DOF transcription factor BPBF in the regulation of gibberellin-responsive genes in barley aleurone. *Plant. Physiol.* **130**, 111–119.
- Merkouropoulos, G., Barnett, D.C. and Shirsat, A.H. (1999) The *Arabidopsis* extensin gene is developmentally regulated, is induced by wounding, methyl jasmonate, abscisic acid, and codes for a protein with unusual motifs. *Planta*, **208**, 212–219.
- Oñate-Sánchez, L. and Singh, K.B. (2002) Identification of *Arabidopsis* ethylene-responsive element-binding factors with distinct induction kinetics after pathogen infection. *Plant Physiol.* **128**, 1313–1322.
- Papi, M., Sabatini, S., Altamura, M.M., Hennig, L., Schafer, E., Costantino, P. and Vittorioso, P. (2002) Inactivation of the phloem-specific Dof zinc finger gene DAG1 affects response to light and integrity of the testa of *Arabidopsis* seeds. *Plant Physiol.* **128**, 411–417.
- Pelengaris, S., Rudolph, B. and Littlewood, T. (2000) Action of Myc *in vivo* proliferation and apoptosis. *Curr. Opin. Genet. Dev.* **10**, 100–105.
- Penninckx, I.A., Thomma, B.P., Buchala, A., Mettraux, J.P. and Broekaert, W.F. (1998) Concomitant activation of jasmonate and ethylene response pathways is required for induction of plant defensin gene in *Arabidopsis*. *Plant Cell*, **10**, 2103–2113.
- Plesch, G., Ehrhardt, T. and Mueller-Roeber, B. (2001) Involvement of TAAAG elements suggests a role for Dof transcription factors in guard cell-specific gene expression. *Plant J.* **28**, 455–464.
- Rao, M.V., Lee, H., Creelman, R.A., Mullet, J.E. and Davis, K.R. (2000) Jasmonic acid signaling modulates ozone-induced hypersensitive cell death. *Plant Cell*, **12**, 1633–1646.
- Rebeiz, M., Reeves, N.L. and Posakony, J.W. (2002) SCORE: a computational approach to the identification of cis-regulatory modules and target genes in whole-genome sequence data. Site clustering over random expectation. *Proc. Natl. Acad. Sci. USA*, **23**, 9888–9893.
- Sambrook, J., Maniatis, T. and Fritsch, E.F. (1989) *Molecular cloning: a Laboratory Manual*, 2nd edn. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory.
- Schenk, P.M., Kazan, K., Wilson, I., Anderson, J.P., Richmond, T., Somerville, S.C. and Manners, J.M. (2000) Coordinated plant defense responses in *Arabidopsis* revealed by microarray analysis. *Proc. Natl. Acad. Sci. USA*, **97**, 11655–11660.
- Shah, J., Kachroo, P. and Klessig, D.F. (1999) The *Arabidopsis* *ssi1* mutation restores pathogenesis-related gene expression in *npr1* plants and renders defensin gene expression salicylic acid dependent. *Plant Cell*, **11**, 191–206.
- Showalter, A.M., Bell, J.N., Cramer, C.L., Bailey, J.A., Varner, J.E. and Lamb, C.J. (1985) Accumulation of hydroxyproline-rich glycoprotein mRNAs in response to fungal elicitor and infection. *Proc. Natl. Acad. Sci. USA*, **82**, 6551–6555.
- Silva, H., Yoshioka, K., Dooner, H.K. and Klessig, D.F. (1999) Characterization of a new *Arabidopsis* mutant exhibiting enhanced disease resistance. *Mol. Plant Microbe Interact.* **12**, 1053–1063.
- Singh, K.B., Foley, R.C. and Oñate-Sánchez, L. (2002) Transcription factors in plant defense and stress responses. *Curr. Opin. Plant Biol.* **5**, 430–436.
- Staswick, P.E., Su, W. and Howell, H. (1992) Methyl jasmonate inhibition of root growth and induction of a leaf protein are decreased in an *Arabidopsis thaliana* mutant. *Proc. Natl. Acad. Sci. USA*, **89**, 6837–6840.
- Staswick, P.E., Yuen, G.Y. and Lehman, C.C. (1998) Jasmonate signaling mutants of *Arabidopsis* are susceptible to the soil fungus *Pythium irregulare*. *Plant J.* **15**, 747–754.
- Staswick, P.E., Tiryaki, I. and Rowe, M.L. (2002) Jasmonate response locus *JAR1* and several related *Arabidopsis* genes encode enzymes of the firefly luciferase superfamily that show activity on jasmonic, salicylic, and indole-3-acetic acids in an assay for adenylation. *Plant Cell*, **14**, 1405–1405.
- Vicente-Carbajosa, J., Moose, S.P., Parsons, R.L. and Schmidt, R.J. (1997) A maize zinc-finger protein binds the prolamin box in zein gene promoters and interacts with the basic leucine zipper transcriptional activator Opaque2. *Proc. Natl. Acad. Sci. USA*, **94**, 7685–7690.
- Wagner, A. (1999) Genes regulated cooperatively by one or more transcription factors and their identification in whole eukaryotic genomes. *Bioinformatics*, **15**, 776–784.
- Washio, K. (2001) Identification of Dof proteins with implication in the gibberellin-regulated expression of a peptidase gene following the germination of rice grains. *Biochim. Biophys. Acta*, **1520**, 54–62.
- Ward, E.R., Uknes, S.J., Williams, S.C., Dincher, S.S., Wiederhold, D.L., Alexander, D.C., Ahl-Grey, P., Mettraux, J.P. and Ryals, J.A. (1991) Coordinate gene activity in response to agents that induce systemic acquired resistance. *Plant Cell*, **3**, 1085–1094.
- Wesley, S.V., Helliwell, C.A., Smith, N.A. *et al.* (2001) Construct design for efficient, effective and high-throughput gene silencing in plants. *Plant J.* **27**, 581–590.
- Yanagisawa, S. (1996) A novel multigene family that the gene for a maize DNA-binding protein, MNB1a belongs to isolation of

- genomic clones from this family and some aspects of its molecular evolution. *Biochem. Mol. Biol. Int.* **38**, 665–673.
- Yanagisawa, S.** (1997) Dof DNA-binding domains of plant transcription factors contribute to multiple protein–protein interactions. *Eur. J. Biochem.* **250**, 403–410.
- Yanagisawa, S.** (2000) Dof1 and Dof2 transcription factors are associated with expression of multiple genes involved in carbon metabolism in maize. *Plant J.* **21**, 281–288.
- Yanagisawa, S.** (2002) The Dof family of plant transcription factors. *Trends Plant. Sci.* **7**, 555–560.
- Yanagisawa, S. and Schmidt, R.J.** (1999) Diversity and similarity among recognition sequences of Dof transcription factors. *Plant J.* **17**, 209–214.
- Yanagisawa, S. and Sheen, J.** (1998) Involvement of maize Dof zinc finger proteins in tissue-specific and light-regulated gene expression. *Plant Cell*, **10**, 75–89.
- Zhang, B., Chen, W., Foley, R.C., Büttner, M. and Singh, K.B.** (1995) Interactions between distinct types of DNA-binding proteins enhance binding to ocs element promoter sequences. *Plant Cell*, **7**, 2241–2252.